

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Wang et al.

Art Unit: Not yet assigned

Application No. Not yet assigned

Filed: Herewith

For: CYCLIN-DEPENDENT KINASE
INHIBITORS AS PLANT GROWTH
REGULATORS

Examiner: Not yet assigned

Date: December 8, 2000

STATEMENT IN COMPLIANCE WITH 37 C.F.R. § 1.821(f)

TO THE COMMISSIONER FOR PATENTS

Washington, DC 20231

Sir:

In compliance with 37 C.F.R. § 1.821(f), the undersigned declares that the nucleotide and/or amino acid sequences presented in the paper copy of the "Sequence Listing" submitted herewith are the same as the sequences contained in the computer-readable form of the "Sequence Listing."

Respectfully submitted,

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SEQUENCE LISTING

<110> Agriculture and Agri-Food Canada; The University of Saskatchewan

<120> Cyclin Dependant Kinase Inhibitors as Plant Growth
Regulators

<130> 81601-3

<140>

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<150> CA 2,256,121

<151> 1998-12-31

<160> 16

<170> PatentIn Ver. 2.0

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Ser	Thr	Tyr	Met	Gln	Leu	Arg	Ser	Arg	Arg	Ile	Val	Tyr	Val	Arg	Ser	
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Glu	Lys	Ser	Ser	Ser	Val	Ser	Val	Val	Gly	Asp	Asn	Gly	Val	Ser	Ser	
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 70 75 80

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 Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Glu Lys Glu
 85 90 95

gaa tta agt aaa tcc atg gag aat tat tca tcg gaa ttt gaa tcg gcg 393
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 100 105 110

gtt aaa gaa tcg tta gat tgt tgt tgt agc ggg agg aaa acg atg gag 441
 Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met Glu
 115 120 125

gag acg gtg acg gcg gag gag gag gag aag gcg aaa ttg atg acg gag 489
 Glu Thr Val Thr Ala Glu Glu Glu Glu Lys Ala Lys Leu Met Thr Glu
 130 135 140 145

atg cca acg gaa tcg gaa att gaa gat ttt ttt gtg gaa gct gag aaa 537
 Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu Lys
 150 155 160

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 165 170 175

gag aag cca tta gaa gga cgt tac gaa tgg gta aag tta gag 627
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 180 185 190

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gaataagtta attttatttt gttgatttgg aaatataaga tttgtaggag gaatgttttt 747

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 35 40 45

Ser Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His
 50 55 60

Leu Glu Glu Glu Asp Lys Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg
 65 70 75 80
 Arg Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Glu Lys
 85 90 95
 Glu Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser
 100 105 110
 Ala Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met
 115 120 125
 Glu Glu Thr Val Thr Ala Glu Glu Glu Lys Ala Lys Leu Met Thr
 130 135 140
 Glu Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu
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 aagccattag aaggacgtta cgaatgggta aagttagagt gaagaagaag aagaagttaa 540
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 gaaggagaag ccattagaag gacgttacga atgggtaaag ttagagtga gaagaagaag 360
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tgatgataat gatgatcatt gttttcacca aagtacttat tattttctctt ctgtaataat 600
 ctttgctttg attttttctt taacaaaatc caaatgtaga tatctttctc tcgaataatc 660
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aatttcagga aacaggggaat ttcacatcaagc gagaatctgg gagaaacagc agaaatggac 420
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35 40 45
Ser Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His
50 55 60
Leu Glu Glu Glu Asp Lys Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg
65 70 75 80
Arg Gly Thr Lys Arg Lys Leu Cys Glu Asn Leu Arg Glu Glu Glu Lys
85 90 95

Glu Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser
 100 105 110
 Ala Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met
 115 120 125
 Glu Glu Thr Val Thr Ala Glu Glu Glu Glu Lys Ala Lys Leu Met Thr
 130 135 140
 Glu Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu
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 Lys Ser Lys Arg Arg Ile Glu Phe Val Asp Leu Glu Glu Asn Asn Gly
 65 70 75 80
 Asp Asp Arg Glu Thr Glu Thr Ser Trp Ile Tyr Asp Asp Leu Asn Lys
 85 90 95
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 100 105 110
 Val Glu Ser Arg Arg Arg Leu Arg Lys Ser Leu His Glu Thr Val Lys
 115 120 125
 Glu Ala Glu Leu Glu Asp Phe Phe Gln Val Ala Glu Lys Asp Leu Arg
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 Ser Glu Ser Lys Glu Ile Ala Lys Asn Ser Ser Ser Phe Gly Val Asp
 100 105 110
 Leu Glu Asp His Gln Ile Glu Thr Glu Thr Glu Thr Ser Thr Phe Ile
 115 120 125
 Thr Ser Asn Phe Arg Lys Glu Thr Ser Pro Val Ser Glu Gly Leu Gly
 130 135 140
 Glu Thr Thr Thr Glu Met Glu Ser Ser Ser Ala Thr Lys Arg Lys Gln
 145 150 155 160
 Pro Gly Val Arg Lys Thr Pro Thr Ala Ala Glu Ile Glu Asp Leu Phe
 165 170 175
 Ser Glu Leu Glu Ser Gln Asp Asp Lys Lys Lys Gln Phe Ile Glu Lys
 180 185 190
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 Trp Asp Arg Leu
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Arg Tyr Glu Trp Val Gln Val Lys Pro
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 35 40 45

Leu Glu Val Ala Ala Val Val Glu Glu Glu Glu Val Ala Asn Cys Ser
 50 55 60
 Ser Ser Glu Val Ile Thr Thr Ala Arg Ser Asp Phe Pro Pro Ser Cys
 65 70 75 80
 Cys Ser Ser Asn Tyr Asp Gln Leu Ser Ser Ser Glu Pro Glu Val Val
 85 90 95
 Lys Asp Asp Asp Gly Leu Gly Asn Arg Thr Ala Asp Pro Glu Val Glu
 100 105 110
 Ser Gly Glu Ala Ser Ser Lys Gln Lys Glu Ser His Arg Thr Glu Ala
 115 120 125
 Arg Glu Ala Thr Lys Leu Asp Asp Gln Asp Tyr Pro Ala Thr Lys Ser
 130 135 140
 Thr Val Gln Ile Lys Met Pro Ser Asp Ser Glu Ile Glu Glu Phe Phe
 145 150 155 160
 Ala Val Ala Glu Lys Asp Leu Gln Lys Arg Phe Ser Glu Lys Tyr Asn
 165 170 175
 Phe Asp Ile Val Lys Asp Val Pro Leu Lys Gly Arg Tyr Asp Trp Val
 180 185 190
 Pro Ile Asn Pro
 195

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